A Canine Urinary Tract Infection Representing the First Clinical Veterinary Isolation of Acinetobacter ursingii

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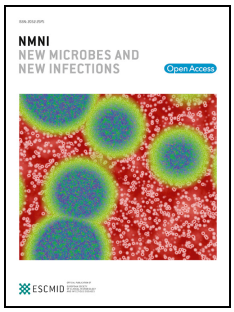

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A Canine Urinary Tract Infection Representing the First Clinical Veterinary Isolation of *Acinetobacter ursingii*

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Abstract

Acinetobacter species can be important opportunistic pathogens in humans, especially in health care settings. We report here the first isolation of *Acinetobacter ursingii* from an animal species where it was isolated from a canine urinary tract infection and where phenotypic identification proved unreliable.

Keywords

canine; *Acinetobacter ursingii*; urinary tract infection; molecular diagnostics; veterinary microbiology;

Acinetobacter species cause a wide range of infections in humans with those most frequently isolated belonging to the *Acinetobacter calcoaceticus-Acinetobacter baumannii* complex (1). While other species are pathogenic, much less is known about their epidemiology and their laboratory identification can be unreliable (2, 3). A Gram-negative bacilli, isolate 76496, was cultured from free catch urine received from an 8.5 year old, male Border Terrier submitted for diagnosis to Easter Bush Pathology, University of Edinburgh. The dog had a previous history of acute kidney injury of unknown origin, resulting in permanent reduction of renal function (chronic kidney disease) and was presented for a routine re-check. The urine culture was pure with a viable count of $>10^6$ cfu/ml. While this does not confirm the isolate as the definite cause of chronic kidney disease and a free catch can be susceptible to contamination, the heavy growth and purity indicates clinical significance. Phenotypic identification using Vitek2 and Analytical Profile Index (API) failed to give a reliable identification. In the case of Vitek2, a 'Low Discrimination' result with the Bionumber: 0040001101501000 was returned using the Gram-negative (GN) identification card. Three possible organisms were listed: *Pseudomonas fluorescens*, *Acinetobacter lwoffii* and *Bordetella bronchiseptica*. A repeat analysis gave the result as 'unidentified' with the similar Bionumber: 0040000101501000. The API 20 NE strip (for non-fastidious, non-enteric Gram-negative rods) gave an 'Acceptable identification to the genus' for *Acinetobacter* with the numerical code 0000071 and *Acinetobacter junii/johnsonii* (63.1%) and *Acinetobacter baumannii/calcoaceticus* (26.1%) given as the significant taxa. 16S rDNA sequencing was therefore used to identify the isolate. A 16S rDNA was amplified by PCR with primers fD1 and rP2 (4) and sequenced on both strands with primers fD1 and rP2, and 519r, 536f, 357f and 1385r (5). Using EzBioCloud (6) this 1402 bp partial 16S sequence yielded a 100% match to that of the *Acinetobacter ursingii* type strain DSM 16037 (Accession AIEA01000080 at positions 29-1430). Susceptibility testing by disc diffusion found the isolate susceptible to all antimicrobials tested: ampicillin, amoxicillin/clavulanate, cephalexin, clindamycin, enrofloxacin, erythromycin, and trimethoprim/sulphonamide. This antibiogram may indicate a possible community/environmental source rather than being nosocomially acquired.

The dog received a 1 week course of amoxicillin/clavulanate, resulting in a negative culture from a follow-up urine sample 10 days after cessation of treatment.

First identified in 2001, *A*. *ursingii* has been isolated from various human infections including urinary tract infection (2, 7, 8). Dortet *et al*. (2) describe similar problems with the phenotypic identification of *A*. *ursingii* to those encountered here, and suggest therefore that the true prevalence of *A*. *ursingii* infection may be underestimated. Notably, $^{9}/_{10}$ of their studied *A*. *ursingii isolates* gave the API 20 NE numerical code of 0000071, identical to our isolate, leading them to propose that such a result represents a 'reasonably reliable' approach to identify *A*. *ursingii* (2). The poor reliably of Vitek2 for the identification of *A*. *ursingii* has also been reported in a further study (3).

This report is the first veterinary isolation of *A*. *ursingii* and this organism must be considered as a possible aetiological agent in veterinary diagnostic laboratories. This is especially the case where phenotypic tests are inconclusive but indicative of an *Acinetobacter* species with identification by molecular approaches advisable. Given the potential for *Acinetobacter* species to carry multi-drug resistance, although that was not the case here, and to cause nosocomial infections it is important for veterinary microbiology to accurately identify these and track their epidemiology.

References

1. Wong D, Nielsen TB, Bonomo RA, Pantapalangkoor P, Luna B, Spellberg B. Clinical and Pathophysiological Overview of *Acinetobacter* Infections: a Century of Challenges. Clin Microbiol Rev. 2017;30(1):409-47.
2. Dortet L, Legrand P, Soussy C-J, Cattoir V. Bacterial Identification, Clinical Significance, and Antimicrobial Susceptibilities of *Acinetobacter ursingii* and *Acinetobacter schindleri*, Two Frequently Misidentified Opportunistic Pathogens. Journal of Clinical Microbiology. 2006;44(12):4471-8.
3. Chiu C-H, Lee Y-T, Wang Y-C, Yin T, Kuo S-C, Yang Y-S, et al. A retrospective study of the incidence, clinical characteristics, identification, and antimicrobial susceptibility of bacteremic isolates of *Acinetobacter ursingii*. BMC Infectious Diseases. 2015;15(1):400.
4. Weisburg WG, Barns SM, Pelletier DA, Lane DJ. 16S ribosomal DNA amplification for phylogenetic study. Journal of Bacteriology. 1991;173(2):697-703.
5. Rainey FA, Ward-Rainey N, Kroppenstedt RM, Stackebrandt E. The Genus Nocardiopsis Represents a Phylogenetically Coherent Taxon and a Distinct Actinomycete Lineage: Proposal of *Nocardiopsaceae* fam. nov. International Journal of Systematic and Evolutionary Microbiology. 1996;46(4):1088-92.
6. Yoon S-H, Ha S-M, Kwon S, Lim J, Kim Y, Seo H, et al. Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. International Journal of Systematic and Evolutionary Microbiology. 2017;67(5):1613-7.
7. Nemec A, De Baere T, Tjernberg I, Vaneechoutte M, van der Reijden TJK, Dijkshoorn L. *Acinetobacter ursingii* sp nov and *Acinetobacter schindleri* sp nov., isolated from human clinical specimens. International Journal of Systematic and Evolutionary Microbiology. 2001;51:1891-9.
8. Turton JF, Shah J, Ozongwu C, Pike R. Incidence of *Acinetobacter* Species Other than *A. baumannii* among Clinical Isolates of *Acinetobacter*: Evidence for Emerging Species. Journal of Clinical Microbiology. 2010;48(4):1445-9.